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#66 Search flavivirus replicon		20:49:15	64
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#71 Search flavivirus backbone envelope		20:48:58	13
#70 Search flavivirus backbone		20:48:53	25
#69 Search flavivirus yellow fever west nile		20:48:20	156
#67 Search flavivirus yellow fever		20:48:12	965
#64 Search flavivirus envelope protein		20:47:02	294
#63 Search flavivirus green fluorescent protein		20:46:52	15
#62 Search flavivirus green		20:46:42	84
#61 Search flavivirus GFP		20:46:37	16
#60 Search flavivirus IRES		20:46:30	16
#59 Search flavivirus DNA promoter		20:46:21	26
#58 Search flavivirus DNA reporter		20:46:16	12
#57 Search west nile DNA reporter		20:46:10	4
#56 Search flavivirus west nile DNA reporter		20:46:06	4
#55 Search flavivirus west nile DNA lineage		20:45:49	3
#54 Search flavivirus west nile cDNA		20:45:36	29
#53 Search flavivirus west nile DNA		20:45:31	134
#52 Search flavivirus west nile		20:45:24	1732
#51 Search flavivirus		20:45:20	8468

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May 22 2006 06:31:57

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
S1	1525	west adj nile	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:30
S2	8751	replicon\$	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/21 20:13
S3	126	S1 and S2	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/21 20:16
S4	908	reverse adj genetic\$	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/21 20:16
S5	101781	cDNA	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:30
S6	1526	west adj nile	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:30
S7	723	S6 and S5	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31
S8	424531	delet\$	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31
S9	614	S7 and S8	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31

EAST Search History

S10	300806	envelope\$	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31
S11	473	S9 and S10	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31
S12	182065	promoter	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31
S13	55207	reporter	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:31
S14	324	S11 and S12 and S13	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 20:10
S15	356598	ires	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:32
S16	35	S14 and S15	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 18:32
S17	910	reverse adj genetics	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 20:10
S18	3829	flavivir\$	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 20:11
S19	74	S17 and S18	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2006/05/23 20:11



results of BLAST

BLASTN 2.2.14 [May-07-2006]
RID: 1148512175-2216-116532263996.BLASTQ1

Database: env_nt
1,047,779 sequences; 1,063,283,128 total letters

Query=
Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: environmental samples
Posted date: May 19, 2006 3:31 AM
Number of letters in database: 1,063,283,128
Number of sequences in database: 1,047,779
Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 1047779
Number of Hits to DB: 17877
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 11020
Length of database: 1063283128
Length adjustment: 32
Effective length of query: 10988
Effective length of database: 1029754200
Effective search space: 11314939149600
Effective search space used: 11314939149600
A: 0
X1: 13 (25.0 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 13 (25.1 bits)
S2: 22 (41.7 bits)



results of BLAST

BLASTN 2.2.14 [May-07-2006]
RID: 1148511929-7071-210325148673.BLASTQ4

Database: Whole-Genome-Shotgun Sequences
13,679,503 sequences; 71,237,490,689 total letters

Query=
Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: Whole-Genome-Shotgun Sequences
Posted date: May 18, 2006 7:42 PM
Number of letters in database: -1,837,793,559
Number of sequences in database: 13,677,712
Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 13677712
Number of Hits to DB: 1564364
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 11020
Length of database: 71176650469
Length adjustment: 37
Effective length of query: 10983
Effective length of database: 70670575125
Effective search space: 776174926597875
Effective search space used: 776174926597875
A: 0
X1: 16 (30.8 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 16 (30.7 bits)
S2: 25 (47.3 bits)



results of BLAST

```

# BLASTN 2.2.14 [May-07-2006]
# Query:
# Database: nr
# Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q
# 100 hits found
1_797 gi|21929238|gb|AF404756.1| 99.84 11029 9 5 1 11020
1_797 gi|11597239|gb|AF196835.2|AF196835 99.78 11029 15 5 1
1_797 gi|21929234|gb|AF404754.1| 99.76 11029 18 5 1 11020
1_797 gi|9930133|gb|AF260967.1|AF260967 99.76 11029 18 5 1
1_797 gi|77980183|gb|AY848696.2| 99.75 11029 19 5 1 11020
1_797 gi|50838784|dbj|AB185917.1| 99.75 11029 19 5 1 11020
1_797 gi|50838782|dbj|AB185916.1| 99.75 11029 19 5 1 11020
1_797 gi|75859185|gb|AY842931.3| 99.74 11029 20 5 1 11020
1_797 gi|50872124|dbj|AB185914.2| 99.74 11029 20 5 1 11020
1_797 gi|77980181|gb|AY848695.2| 99.73 11029 21 5 1 11020
1_797 gi|77166600|gb|DQ211652.1| 99.73 11029 21 5 1 11020
1_797 gi|76781535|gb|DQ164188.1| 99.72 11029 22 5 1 11020
1_797 gi|50872125|dbj|AB185915.2| 99.72 11029 22 5 1 11020
1_797 gi|66735926|gb|DQ066423.1| 99.71 11029 23 5 1 11020
1_797 gi|77853218|gb|AY848697.2| 99.70 11029 24 5 1 11020
1_797 gi|21929236|gb|AF404755.1| 99.70 11029 24 5 1 11020
1_797 gi|21929232|gb|AF404753.1| 99.70 11029 24 5 1 11020
1_797 gi|76781547|gb|DQ164194.1| 99.66 11029 28 5 1 11020
1_797 gi|76781559|gb|DQ164200.1| 99.65 11029 30 5 1 11020
1_797 gi|26284711|gb|AF533540.1| 99.65 11029 30 5 1 11020
1_797 gi|76781531|gb|DQ164186.1| 99.64 11029 31 5 1 11020
1_797 gi|55669121|gb|AY646354.1| 99.64 11030 30 6 1 11020
1_797 gi|76781549|gb|DQ164195.1| 99.64 11029 31 5 1 11020
1_797 gi|76781545|gb|DQ164193.1| 99.64 11029 31 5 1 11020
1_797 gi|59876232|gb|AY795965.1| 99.62 11029 33 5 1 11020
1_797 gi|76781541|gb|DQ164191.1| 99.60 11029 35 5 1 11020
1_797 gi|76781571|gb|DQ164206.1| 99.59 11030 34 7 1 11020
1_797 gi|76781569|gb|DQ164205.1| 99.59 11029 36 5 1 11020
1_797 gi|76781555|gb|DQ164198.1| 99.59 11029 36 5 1 11020
1_797 gi|76781553|gb|DQ164197.1| 99.59 11029 36 5 1 11020
1_797 gi|76781533|gb|DQ164187.1| 99.58 11029 37 5 1 11020
1_797 gi|55495180|gb|AY712948.1| 99.57 11029 38 5 1 11020
1_797 gi|71483604|gb|DQ080053.1| 99.57 11029 38 5 1 11020
1_797 gi|76781551|gb|DQ164196.1| 99.56 11029 39 5 1 11020
1_797 gi|55495165|gb|AY712947.1| 99.56 11029 39 5 1 11020
1_797 gi|19387527|gb|AF481864.1| 99.56 11029 39 5 1 11020
1_797 gi|71483602|gb|DQ080052.1| 99.56 11029 39 5 1 11020
1_797 gi|76781557|gb|DQ164199.1| 99.56 11029 39 5 1 11020
1_797 gi|76781537|gb|DQ164189.1| 99.56 11029 39 5 1 11020
1_797 gi|71483600|gb|DQ080051.1| 99.56 11029 40 5 1 11020
1_797 gi|7717200|gb|AF206518.2|AF206518 99.72 10975 22 5 19
1_797 gi|76781543|gb|DQ164192.1| 99.56 11029 40 5 1 11020
1_797 gi|33948906|gb|AY289214.1| 99.54 11029 42 5 1 11020
1_797 gi|76781539|gb|DQ164190.1| 99.54 11029 42 5 1 11020
1_797 gi|71483606|gb|DQ080054.1| 99.52 11029 44 5 1 11020
1_797 gi|76781563|gb|DQ164202.1| 99.51 11029 45 5 1 11020
1_797 gi|71483614|gb|DQ080058.1| 99.51 11029 45 5 1 11020
1_797 gi|71483640|gb|DQ080071.1| 99.59 11000 36 5 30 11020
1_797 gi|76781567|gb|DQ164204.1| 99.50 11029 46 5 1 11020
1_797 gi|55495130|gb|AY712945.1| 99.49 11029 47 5 1 11020
1_797 gi|71483608|gb|DQ080055.1| 99.52 11018 44 5 1 11009
1_797 gi|71483622|gb|DQ080062.1| 99.55 11001 40 5 29 11020

```

1_797	gi 76781565 gb DQ164203.1	99.46	11029	51	5	1	11020
1_797	gi 55495149 gb AY712946.1	99.47	11029	50	5	1	11020
1_797	gi 71483634 gb DQ080068.1	99.54	11001	42	5	29	11020
1_797	gi 71483616 gb DQ080059.1	99.46	11029	51	5	1	11020
1_797	gi 71483630 gb DQ080066.1	99.54	11001	42	5	29	11020
1_797	gi 76781561 gb DQ164201.1	99.45	11029	52	5	1	11020
1_797	gi 71483632 gb DQ080067.1	99.53	11001	43	5	29	11020
1_797	gi 71483610 gb DQ080056.1	99.47	11019	49	5	1	11010
1_797	gi 71483642 gb DQ080072.1	99.53	11000	43	5	30	11020
1_797	gi 71483620 gb DQ080061.1	99.53	11000	43	5	30	11020
1_797	gi 71483636 gb DQ080069.1	99.60	10975	35	5	29	10994
1_797	gi 71483626 gb DQ080064.1	99.52	11001	44	5	29	11020
1_797	gi 71483628 gb DQ080065.1	99.53	10995	43	5	35	11020
1_797	gi 71483638 gb DQ080070.1	99.50	11001	46	5	29	11020
1_797	gi 6581069 gb AF202541.1 AF202541	99.66	10946	26	7	43	
1_797	gi 55975602 gb AY660002.1	99.40	11029	57	5	1	11020
1_797	gi 71483624 gb DQ080063.1	99.53	10975	43	5	29	10994
1_797	gi 71483612 gb DQ080057.1	99.53	10956	43	5	1	10947
1_797	gi 71483618 gb DQ080060.1	99.42	10972	55	5	30	10992
1_797	gi 89148117 gb DQ118127.1	99.12	10969	87	5	1	10960
1_797	gi 33242576 gb AY268133.1	97.97	10990	212	7	21	11000
1_797	gi 30349729 gb AY278441.1	97.27	11001	285	11	1	10989
1_797	gi 89340493 gb DQ411029.1	97.24	10816	280	15	24	10825
1_797	gi 89340495 gb DQ411030.1	97.22	10814	286	11	24	10825
1_797	gi 89340778 gb DQ411031.1	97.21	10814	287	11	24	10825
1_797	gi 87116126 gb DQ377180.1	97.20	10815	286	13	24	10825
1_797	gi 89340786 gb DQ411035.1	97.18	10815	288	13	24	10825
1_797	gi 87083862 gb DQ374652.1	97.23	10793	282	13	24	10803
1_797	gi 89340784 gb DQ411034.1	97.17	10816	287	15	24	10825
1_797	gi 87116124 gb DQ377179.1	97.17	10815	289	13	24	10825
1_797	gi 9930137 gb AF260969.1 AF260969	96.55	11030	369	7	1	
1_797	gi 87116122 gb DQ377178.1	97.16	10816	288	15	24	10825
1_797	gi 87083860 gb DQ374651.1	97.16	10815	290	13	24	10825
1_797	gi 87083864 gb DQ374653.1	97.12	10815	295	13	24	10825
1_797	gi 87083858 gb DQ374650.1	97.12	10815	295	13	24	10825
1_797	gi 89340782 gb DQ411033.1	97.11	10813	299	9	24	10825
1_797	gi 89340780 gb DQ411032.1	97.08	10815	299	13	24	10825
1_797	gi 30230630 gb AY262283.1	96.50	10986	373	8	37	11012
1_797	gi 21929240 gb AF404757.1	96.35	11030	392	7	1	11020
1_797	gi 12744408 gb AF317203.1 AF317203	96.41	10974	381	9	33	
1_797	gi 51011373 gb AY701412.1	96.48	10946	374	7	43	10978
1_797	gi 33242574 gb AY268132.1	96.34	10989	393	5	21	11000
1_797	gi 51011375 gb AY701413.1	96.23	10950	394	15	43	10978
1_797	gi 30349727 gb AY277252.1	96.36	10847	382	9	1	10836
1_797	gi 30349731 gb AY278442.1	96.35	10844	383	9	1	10833
1_797	gi 9930135 gb AF260968.1 AF260968	95.35	11036	490	19	1	
1_797	gi 46277828 gb AY490240.2	95.21	11043	491	34	1	11020
1_797	gi 51318183 gb AY603654.1	94.70	11041	552	29	1	11020



results of BLAST

BLASTN 2.2.14 [May-07-2006]
RID: 1148511147-28338-105062820528.BLASTQ1

Database: NCBI Transcript Reference Sequences
652,821 sequences; 1,111,501,987 total letters

Query=
Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: NCBI Transcript Reference Sequences
Posted date: May 18, 2006 10:45 PM
Number of letters in database: 1,111,494,313
Number of sequences in database: 652,832
Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 652832
Number of Hits to DB: 522
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 11020
Length of database: 1111494313
Length adjustment: 32
Effective length of query: 10988
Effective length of database: 1090603689
Effective search space: 11983553334732
Effective search space used: 11983553334732
A: 0
X1: 14 (26.9 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 14 (27.0 bits)
S2: 22 (41.7 bits)



results of BLAST

```
# BLASTN 2.2.14 [May-07-2006]
# Query:
# Database: refseq_genomic
# Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q
# 6 hits found
1_11050 gi|11528013|ref|NC_001563.2|    79.51    8278    1437    249      1    8153
1_11050 gi|11528013|ref|NC_001563.2|    90.77    509     37      10    10516   11020
1_11050 gi|9626460|ref|NC_001437.1|    72.46    3242    622     260      577   3684
1_11050 gi|9626460|ref|NC_001437.1|   100.00     28      0       0    10789   10816
1_11050 gi|56692441|ref|NC_006551.1|   76.88    558     60      53    10496   11020
1_11050 gi|9626685|ref|NC_001477.1|   86.75    83      9       2    9040    9121
```



results of BLAST

BLASTN 2.2.14 [May-07-2006]
 RID: 1148511003-17158-142892004559.BLASTQ4

Database: Genome Survey Sequence, includes single-pass genomic data, exon-trapped sequences, and Alu PCR sequences.

14,335,827 sequences; 9,038,742,965 total letters

Query=
 Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: Genome Survey Sequence, includes single-pass genomic data, exon-trapped sequences, and Alu PCR sequences.

Posted date: May 18, 2006 8:24 PM

Number of letters in database: 446,610,113

Number of sequences in database: 14,332,659

Lambda K H
 1.33 0.621 1.12

Gapped

Lambda K H
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 14332659

Number of Hits to DB: 171244

Number of extensions: 0

Number of successful extensions: 0

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 0

Number of HSP's successfully gapped: 0

Length of query: 11020

Length of database: 9036544705

Length adjustment: 34

Effective length of query: 10986

Effective length of database: 8549234299

Effective search space: 93921888008814

Effective search space used: 93921888008814

A: 0

X1: 12 (23.1 bits)

X2: 32 (59.1 bits)

X3: 54 (99.7 bits)

S1: 12 (23.3 bits)

S2: 23 (43.6 bits)



results of BLAST

BLASTN 2.2.14 [May-07-2006]
RID: 1148511297-13266-29868804930.BLASTQ4

Database: Unfinished High Throughput Genomic Sequences; Sequences:
phases 0,1 and 2
91,378 sequences; 15,441,179,013 total letters

Query=
Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: Unfinished High Throughput Genomic Sequences; Sequences: phases 0,1 and 2
Posted date: May 18, 2006 11:01 PM
Number of letters in database: -1,740,329,326
Number of sequences in database: 91,362
Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 91362
Number of Hits to DB: 330308
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 11020
Length of database: 15439539854
Length adjustment: 35
Effective length of query: 10985
Effective length of database: 15436342184
Effective search space: 169568218891240
Effective search space used: 169568218891240
A: 0
X1: 19 (36.5 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 19 (36.2 bits)
S2: 24 (45.4 bits)



results of BLAST

```

# BLASTN 2.2.14 [May-07-2006]
# Query:
# Database: pat
# Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q
# 44 hits found
1_12764 gi|27647035|emb|AX577796.1| 99.56 11029 39 5 1 11020
1_12764 gi|27646162|emb|AX576542.1| 99.56 11029 39 5 1 11020
1_12764 gi|52747867|emb|CQ874691.1| 99.81 2070 4 0 400 2469
1_12764 gi|52745306|emb|CQ871188.1| 99.81 2070 4 0 400 2469
1_12764 gi|51997335|emb|CQ867049.1| 99.81 2070 4 0 400 2469
1_12764 gi|15554477|emb|AX224225.1| 99.85 2008 3 0 421 2428
1_12764 gi|44845960|emb|CQ754934.1| 99.73 1483 4 0 918 2400
1_12764 gi|44845959|emb|CQ754933.1| 99.73 1483 4 0 918 2400
1_12764 gi|44845215|emb|CQ753913.1| 99.73 1483 4 0 918 2400
1_12764 gi|44845214|emb|CQ753912.1| 99.73 1483 4 0 918 2400
1_12764 gi|52747866|emb|CQ874690.1| 99.78 1375 3 0 918 2292
1_12764 gi|44845219|emb|CQ753917.1| 99.78 1375 3 0 918 2292
1_12764 gi|52747868|emb|CQ874692.1| 99.91 1101 1 0 2401 3501
1_12764 gi|44845961|emb|CQ754935.1| 99.91 1101 1 0 2401 3501
1_12764 gi|44845216|emb|CQ753914.1| 99.91 1101 1 0 2401 3501
1_12764 gi|3964470|gb|AR003211.1|AR003211 72.49 3243 619 261 577
1_12764 gi|3964377|gb|AR003118.1|AR003118 72.49 3243 619 261 577
1_12764 gi|588599|gb|I08692.1| 72.45 3245 620 262 577 3684 274
1_12764 gi|2170697|dbj|E02466.1| 72.16 3261 637 262 558 3684
1_12764 gi|2170908|dbj|E02680.1| 72.16 3261 637 262 558 3684
1_12764 gi|92829674|dbj|DD136821.1| 100.00 201 0 0 1028 1228
1_12764 gi|55581982|emb|CQ897149.1| 96.17 183 0 5 10845 11020
1_12764 gi|55581981|emb|CQ897148.1| 97.00 100 1 2 10553 10650
1_12764 gi|55581943|emb|CQ897110.1| 80.33 244 25 21 10708 10946
1_12764 gi|55581947|emb|CQ897114.1| 79.92 244 26 21 10708 10946
1_12764 gi|55581945|emb|CQ897112.1| 79.92 244 26 21 10708 10946
1_12764 gi|55581939|emb|CQ897106.1| 79.92 244 26 21 10708 10946
1_12764 gi|55581950|emb|CQ897117.1| 79.84 243 26 21 10708 10945
1_12764 gi|55581948|emb|CQ897115.1| 80.00 235 25 20 10708 10937
1_12764 gi|55581944|emb|CQ897111.1| 79.59 245 25 22 10708 10946
1_12764 gi|55581949|emb|CQ897116.1| 80.35 229 22 20 10708 10930
1_12764 gi|55581946|emb|CQ897113.1| 79.57 235 26 20 10708 10937
1_12764 gi|55581941|emb|CQ897108.1| 79.27 246 24 25 10708 10946
1_12764 gi|55581942|emb|CQ897109.1| 82.88 111 10 9 10708 10817
1_12764 gi|55581940|emb|CQ897107.1| 82.88 111 10 9 10708 10817
1_12764 gi|55581920|emb|CQ897087.1| 98.08 52 0 1 10905 10955
1_12764 gi|55581919|emb|CQ897086.1| 98.08 52 0 1 10905 10955
1_12764 gi|27646165|emb|AX576545.1| 88.24 51 4 2 433 482
1_12764 gi|88500611|dbj|DD219684.1| 100.00 30 0 0 403 432
1_12764 gi|27646167|emb|AX576547.1| 100.00 29 0 0 10992 11020
1_12764 gi|15554499|emb|AX224249.1| 100.00 29 0 0 421 449
1_12764 gi|27646166|emb|AX576546.1| 100.00 28 0 0 1 28
1_12764 gi|83410046|emb|CS196074.1| 100.00 28 0 0 10616 10643
1_12764 gi|55581931|emb|CQ897098.1| 100.00 25 0 0 10791 10815

```



results of BLAST

BLASTN 2.2.14 [May-07-2006]
RID: 1148511540-26048-113003772134.BLASTQ4

Database: PDB nucleotide database
6378 sequences; 414,729 total letters

Query=
Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: PDB nucleotide database
Posted date: May 18, 2006 10:45 PM
Number of letters in database: 412,402
Number of sequences in database: 6,326
Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 6326
Number of Hits to DB: 53
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 11020
Length of database: 412402
Length adjustment: 22
Effective length of query: 10998
Effective length of database: 273230
Effective search space: 3004983540
Effective search space used: 3004983540
A: 0
X1: 9 (17.3 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 9 (17.7 bits)
S2: 15 (28.8 bits)



results of BLAST

```
# BLASTN 2.2.14 [May-07-2006]
# Query:
# Database: month
# Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q
# 6 hits found
1_20047 gi|95140176|emb|AJ965631.1|    97.32    149      4      0      9122    9270
1_20047 gi|95140170|emb|AJ965628.1|    97.32    149      4      0      9122    9270
1_20047 gi|95140168|emb|AJ965627.1|    97.32    149      4      0      9122    9270
1_20047 gi|95140166|emb|AJ965626.1|    97.32    149      4      0      9122    9270
1_20047 gi|95140174|emb|AJ965630.1|    96.64    149      5      0      9122    9270
1_20047 gi|95140172|emb|AJ965629.1|    96.64    149      5      0      9122    9270
```



results of BLAST

BLASTN 2.2.14 [May-07-2006]
RID: 1148511630-30931-14826378846.BLASTQ1

Database: dbsts
881,195 sequences; 495,721,948 total letters

Query=
Length=11020

No significant similarity found. For reasons why, [click here](#).

Database: Database of GenBank+EMBL+DDBJ sequences from STS Divisions
Posted date: May 19, 2006 5:11 AM
Number of letters in database: 495,721,948
Number of sequences in database: 881,195
Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 881195
Number of Hits to DB: 20596
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 11020
Length of database: 495721948
Length adjustment: 31
Effective length of query: 10989
Effective length of database: 468404903
Effective search space: 5147301479067
Effective search space used: 5147301479067
A: 0
X1: 12 (23.1 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 12 (23.3 bits)
S2: 21 (39.9 bits)



results of BLAST

```
# BLASTN 2.2.14 [May-07-2006]
# Query:
# Database: chromosome
# Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q
# 6 hits found
1_26437 gi|11528013|ref|NC_001563.2|    79.51    8278    1437    249      1    8153
1_26437 gi|11528013|ref|NC_001563.2|    90.77    509     37      10    10516   11020
1_26437 gi|9626460|ref|NC_001437.1|    72.46    3242    622     260      577   3684
1_26437 gi|9626460|ref|NC_001437.1|   100.00     28      0       0    10789   10816
1_26437 gi|56692441|ref|NC_006551.1|   76.88    558     60      53    10496   11020
1_26437 gi|9626685|ref|NC_001477.1|   86.75    83      9       2    9040    9121
```